Amendments to the Claims

This listing of claims will replace all prior versions and listings of all claims in the application.

Claims 1-3 (cancelled)

4. (Currently amended) A method for generating a ~~secondary~~ tertiary library of scaffold protein variants comprising:

a) inputting into a computer a plurality of primary sequences and a scaffold protein sequence;

b) generating a library of primary sequences utilizing an alignment program;

~~b~~c) generating a probability distribution of amino acid residues in a plurality of primary variant positions from said primary sequences;

~~c~~d) computationally combining a plurality of said amino acid residues from said probability distribution to generate a secondary library of secondary sequences, wherein at least one of said secondary sequences is different from said primary sequences;

~~d~~e) computationally ranking said secondary library and eliminating at least one unfavorably ~~e~~ ranked sequence from said secondary library to generate a tertiary library, wherein at least one sequence of said tertiary library is different from said primary sequences; and

~~e~~f) synthesizing a plurality of tertiary sequences to generate said tertiary library of scaffold protein variants.

5. (Original) A method according to claim 4 wherein said synthesizing is done by multiple PCR with pooled oligonucleotides.

6. (Original) A method according to 5 wherein said pooled oligonucleotides are added in equimolar amounts.

7. (Currently Amended) A method according to claim 5 wherein said pooled oligonucleotides are added in amounts that correspond to the frequency of the amino acid residues from said probability distribution.

8. (Original) A method according to claim 6 wherein said pooled oligonucleotides are pooled in relative amounts.

9. (Currently amended) A method for generating a secondary library of scaffold protein variants comprising:

a) inputting into a computer a plurality of primary sequences and a scaffold protein sequence;

b) generating a library of primary sequences utilizing an alignment program;

~~b~~c) generating a probability distribution of amino acid residues in a plurality of primary variant positions from said primary sequences;

~~c~~d) combining a plurality of said amino acid residues from said probability distribution to generate a secondary library of secondary sequences, wherein at least one of said secondary sequences is different from said primary sequences; and

~~d~~e) synthesizing a plurality of said secondary sequences to generate a secondary library of scaffold protein variants.